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FIG. 1A TECH CENTER 1600/2900

1 CCCACGCGTCCGGGGAGCTTGCACTAACATCTACAATGGCTTCTAAAAAGCACAGATGAC 60

61 CTGCTACACTTCCTGACTTGCTTGCTATTGGTTGGCACTGTTTCATAAATATAATTTGCTC 120

121 TTTCACCTTTTCTTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA 180

181 GAGGCAGCAGAAGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG 240

241 CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTTGAC 300

301 TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCATTTGAT 360

361 AAGGGAAAACCTAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT 420

421 GTGAGCAACGTGGAAGATGGGTGATTTCTGCATTTCCAACCTGAGCATGGAGAGAAAAATT 480

481 TATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA 540

1 M E P N G T F S N 9

541 TAACAACAGCAGGAACTGCACAATTGAAAACCTCAAGAGAGAATTTTTCCCAATTGTATA 600

10 N N S R N C T I E N F K R E F F P I V Y 29

601 TCTGATAATATTTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTTCTGCA 660

30 L I I F F W G V L G N G L S I Y V F L Q 49

661 GCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTGGCCATTTTCAGATCT 720

50 P Y K K S T S V N V F M L N L A I S D L 69

721 CCTGTTTATAAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGAT 780

70 L F I S T L P F R A D Y Y L R G S N W I 89

781 ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAG 840

90 F G D L A C R I M S Y S L Y V N M Y S S 109

841 TATTTATTTCTGACCGTGCTGAGTGTTGTGCGTTTCCTGGCAATGGTTACACCCCTTTTCG 900

110 I Y F L T V L S V V R F L A M V H P F R 129

FIG. 2A

	1	50
HGPRBMY11	(1) -----MSLQPSISVSEMEPNC-----TFSNNNSRNCPTEN--FK	
HGPRBMY11v1	(1) MERKFMSLQPSISVSEMEPNC-----TFSNNNSRNCPTEN--FK	
P2Y5_CHICK	(1) -----MVSNCSTEDS--FK	
P2YR_CHICK	(1) MTEALISAALNGQPETLAGC-----WAAGNATKCSITKTGFO	
P2YR_MELGA	(1) MTEALISAALNGQPETLAGC-----WAAGNATKCSITKTGFO	
P2YR_RAT	(1) MTEVPWSAVPNGDAAFLAGLGSLWGNSTIASAAVSSSFRCAITKTGFO	
Q9Y271	(1) -----MDETC-----NLTVSSATCHDTIDDFR	
GPRH_HUMAN	(1) -----MNGLEVAPP-----LITNFSIATAEQCGQETPLE	
	51	100
HGPRBMY11	(22) REFFPIVYLLIFFWCVLGNGLSTYVFLQPYKKSTSVNVFMENLAISDLLF	
HGPRBMY11v1	(38) REFFPIVYLLIFFWCVLGNGLSTYVFLQPYKKSTSVNVFMENLAISDLLF	
P2Y5_CHICK	(14) YTLXGCVESMVVFILGFTANGVAITYFFITLKVRETTTYMENLAISDLLF	
P2YR_CHICK	(40) EYMLPTVYLLVFITGFLGNSVAIWMFVFMHMPWSGISVYMNLAIADELY	
P2YR_MELGA	(40) EYMLPTVYLLVFITGFLGNSVAIWMFVFMHMPWSGISVYMNLAIADELY	
P2YR_RAT	(51) EYMLPAVYLLVFITGFLGNSVAIWMFVFMHMPWSGISVYMNLAIADELY	
Q9Y271	(23) NQVYSTLYSMTSIVGFGNGFVLYVLLKTYHKKSFAFOVYMNLAIADELY	
GPRH_HUMAN	(31) NMTEASFYLLDFILALVGNFLALWLEFTRDHKSGTPANVFLMHLAVADLSC	
	101	150
HGPRBMY11	(72) ESTLPPFRADYYIRGSNNWIFGDLACRTMSVSLYVNMYSSTYFLTIVLSVVR	
HGPRBMY11v1	(88) ESTLPPFRADYYIRGSNNWIFGDLACRTMSVSLYVNMYSSTYFLTIVLSVVR	
P2Y5_CHICK	(64) VETLPPFRADYYIRGSNNWIFGDLACRTMSVSLYVNMYSSTYFLTIVLSVVR	
P2YR_CHICK	(90) VLTLPALIEYYFNKLDWIFGDMCKLQRFIFHVNLYGSILFLTCISVHRY	
P2YR_MELGA	(90) VLTLPALIEYYFNKLDWIFGDMCKLQRFIFHVNLYGSILFLTCISVHRY	
P2YR_RAT	(101) VLTLPALIEYYFNKLDWIFGDMCKLQRFIFHVNLYGSILFLTCISVHRY	
Q9Y271	(73) VCTLPLRVVYVHKGINLFGDFLCRLSTYALYVNLVYCSIFMTAMSFRC	
GPRH_HUMAN	(81) VLVLPTRLEVYHFGSNHWPFCEIACRLTGFLFYENMYASTYFLTICISADRF	
	151	200
HGPRBMY11	(122) LAMVHPFRLHVTISIRSAWILCGTIWILIMASSIMLLDS---CSEONGSV	
HGPRBMY11v1	(138) LAMVHPFRLHVTISIRSAWILCGTIWILIMASSIMLLDS---CSEONGSV	
P2Y5_CHICK	(113) LAIVHPERSKTLRTKRNARIVCVAVWITVLACSTPASEFFQSTNRONNTEQ	
P2YR_CHICK	(140) TGVVHPLKSLGRLEKKNAVYVSSLVVALVAVIAPILFYSGTCVRNKTI	
P2YR_MELGA	(140) TGVVHPLKSLGRLEKKNAVYVSSLVVALVAVIAPILFYSGTCVRNKTI	
P2YR_RAT	(151) SGVVYPLKSLGRLEKKNAVYVSVLVVLIIVVAISPILFYSGTCIRKNKTV	
Q9Y271	(123) LAIVFPVONTINLVTKKAREVCVGTWIEVILTSSPFLMAKPQKDEKNNTK	
GPRH_HUMAN	(131) LAIVHPVKSLKERRPLYAHLACFLWVWVAVAMAPLLVSPQTVQTNHTVV	
	201	250
HGPRBMY11	(169) TSCLE--LNLYKIAKEQTMNYIALVVGCLPPFETTSICVLLIIRVLLKVE	
HGPRBMY11v1	(185) TSCLE--LNLYKIAKEQTMNYIALVVGCLPPFETTSICVLLIIRVLLKVE	
P2Y5_CHICK	(163) RTCFENFPESTNKTYISRIITIEIVGFFIPLILNMTCSITVLRNLNPL	
P2YR_CHICK	(190) TCYDT--TADERYRSYFVYSMCHTVFMFCIPFIVILGCVGLIVKALTYKD	
P2YR_MELGA	(190) TCYDT--TADERYRSYFVYSMCHTVFMFCIPFIVILGCVGLIVKALTYKD	
P2YR_RAT	(201) TCYDS--TSDEYRSYFVYSMCHTVFMFCIPFIVILGCVGLIVKALTYKD	
Q9Y271	(173) CFEPP--QDNQTKNHMLLHYVSLFVCFIIPFVILTVCYMTLLGLKKS	
GPRH_HUMAN	(181) CLQLY-----REKASHHALVSLAVAFTEPFITITVTCVLLIIRSLRQGL	

FIG. 2B

		251		300
HGPRBMY11	(217)	VPESGLRVSHRKATTTIIITLIIFFLQFLPYHARTFNL	-----	TIWK
HGPRBMY11v1	(233)	VPESGLRVSHRKATTTIIITLIIFFLQFLPYHARTFNL	-----	TIWK
P2Y5_CHICK	(213)	ILSRNKLS-KKKVKKMFMHVLRCFQVYPYNTLILSLMR	--	TQWIN
P2YR_CHICK	(238)	LDNSPLR---RKSTYVIIVLTIVFAVSYLPEHVMKTNLRARLDFOTPQ		
P2YR_MELGA	(238)	LDNSPLR---RKSTYVIIVLTIVFAVSYLPEHVMKTNLRARLDFOTPQ		
P2YR_RAT	(249)	LDNSPLR---RKSTYVIIVLTIVFAVSYLPEHVMKTNLRARLDFOTPE		
Q9Y271	(221)	MKKNLSS--HKKAIGMTMVTAALVSEFMPYHTQRTTEHLHFLHN	--	ETKP
GPRH_HUMAN	(224)	RVEKRLK---TKAMRMIAVLATFLVCFVYPYHVNRSSVVLHYR	--	SHGAS
		301		350
HGPRBMY11	(261)	GLCKDRLEHKALVITLALAAANACFNPELYYFAGENFKDRLSALRK	GHP	
HGPRBMY11v1	(277)	GLCKDRLEHKALVITLALAAANACFNPELYYFAGENFKDRLSALRK	GHP	
P2Y5_CHICK	(260)	CSVVTAVRTMYPVTLGLAVSNGCFDPIVYVFFSDTNSFLDK	--	KQC--VF
P2YR_CHICK	(285)	CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSR		
P2YR_MELGA	(285)	CAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKSSR		
P2YR_RAT	(296)	CFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATRKASR		
Q9Y271	(267)	QDSVLRMQKSVVITLSLAASNGCFDPILYFFSGENFRKRLS	--	FRKHSL
GPRH_HUMAN	(269)	CATORITLALANRITSLTSLNGALDPIMYFFVAEKFRFALCNLLCGKRL		
		351		379
HGPRBMY11	(311)	KAK-TKCVFQVSVWLKKEIRV	-----	
HGPRBMY11v1	(327)	KAK-TKCVFQVSVWLKKEIRV	-----	
P2Y5_CHICK	(306)	QNT	-----	
P2YR_CHICK	(335)	SEP-NVQSKSEEMTLNILTEYKQNGDTSL		
P2YR_MELGA	(335)	SEP-NVQSKSEEMTLNILTEYKQNGDTSL		
P2YR_RAT	(346)	SEA-NVQSKSEEMTLNILSEFKQNGDTSL		
Q9Y271	(316)	SVT-YVPRKASLPEKGEEICKV	-----	
GPRH_HUMAN	(319)	GPPPSREGKTINSSLSAKSEL	-----	

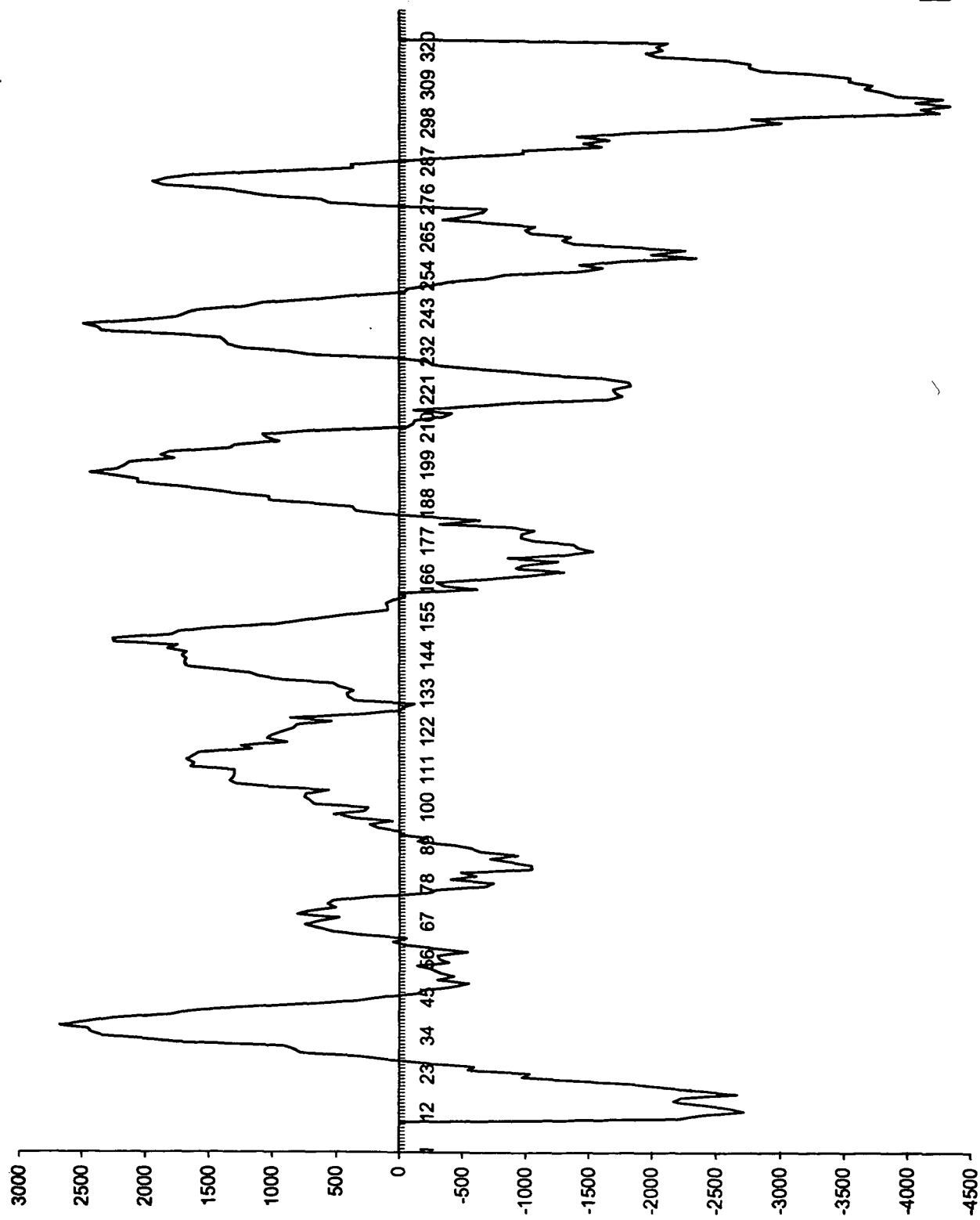


FIG. 3

FIG. 4

Expression Profiling of Novel Human GPCR, HGPRBMY11

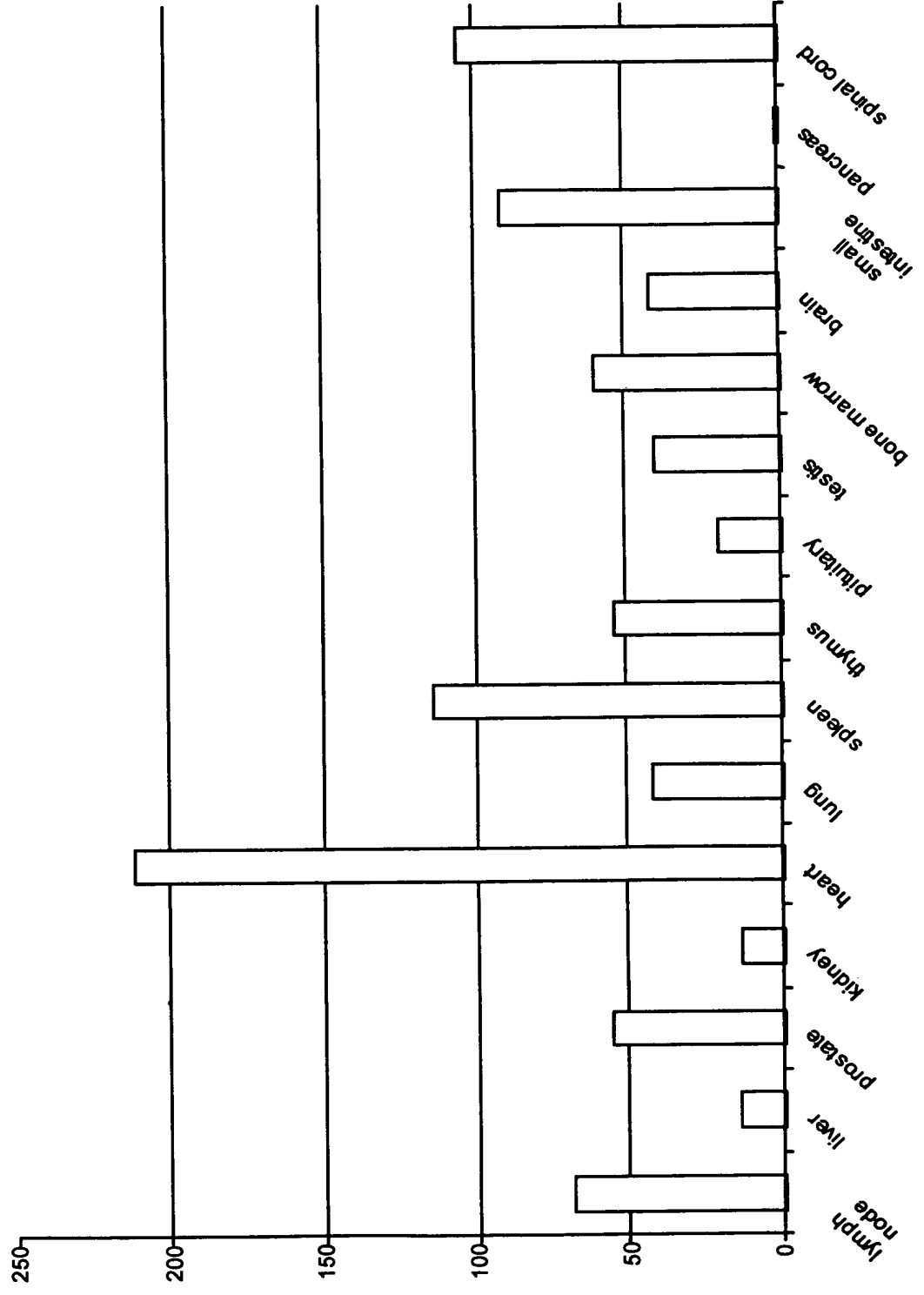


FIG. 5

HGPRBMY11

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37%	49%
chick purinergic receptor 5	gi P32250	36%	46%
human G-protein-coupled receptor GPR17	gi Q13304	36%	46%
chick purinergic receptor	gi P34996	30%	45%
turkey purinergic receptor	gi P49652	30%	45%
rat purinergic receptor	gi P49651	30%	44%

HGPRBMY11v1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37.2%	49%
chick purinergic receptor 5	gi P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi Q13304	36.2%	46.1%
chick purinergic receptor	gi P34996	29.5%	43.9%
turkey purinergic receptor	gi P49652	29.8%	44.2%
rat purinergic receptor	gi P49651	29.6%	44%

FIG. 6A

1 ATGGAGAGAAAAATTTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT 60
 1 M E R K F M S L Q P S I S V S E M E P N 20

 61 GGCACCTTCAGCAATAACAACAGCAGGAAGTGCACAATTGAAAACCTCAAGAGAGAATTT 120
 21 G T F S N N N S R N C T I E N F K R E F 40

 121 TTCCCAATTGTATATCTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATA 180
 41 F P I V Y L I I F F W G V L G N G L S I 60

 181 TATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTTCATGCTAAATCTG 240
 61 Y V F L Q P Y K K S T S V N V F M L N L 80

 241 GCCATTTTCAGATCTCCTGTTTCATAAGCAGCTTCCCTTCAGGGCTGACTATTATCTTAGA 300
 81 A I S D L L F I S T L P F R A D Y Y L R 100

 301 GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGATGTCT 360
 101 G S N W I F G D L A C R I M S Y S L Y V 120

 361 AACATGTACAGCAGTATTTATTTCTGACCGTGTGAGTGTGTGCGTTTCTGGCAATG 420
 121 N M Y S S I Y F L T V L S V V R F L A M 140

 421 GTTCACCCCTTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTGGG 480
 141 V H P F R L L H V T S I R S A W I L C G 160

 481 ATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAG 540
 161 I I W I L I M A S S I M L L D S G S E Q 180

 541 AACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACC 600
 181 N G S V T S C L E L N L Y K I A K L Q T 200

 601 ATGAACTATATTGCCTTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGT 660
 201 M N Y I A L V V G C L L P F F T L S I C 220

 661 TATCTGCTGATCATTTCGGTCTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTT 720
 221 Y L L I I R V L L K V E V P E S G L R V 240

 721 TCTCACAGGAAGGCACTGACCACCATCATCATCACCTTGATCATCTTCTTCTGTGTTTC 780
 241 S H R K A L T T I I I T L I I F F L C F 260

 781 CTGCCCTATCACACACTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAA 840
 261 L P Y H T L R T V H L T T W K V G L C K 280

 841 GACAGACTGCATAAAGCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTC 900
 281 D R L H K A L V I T L A L A A A N A C F 300

FIG. 6B

901	AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTC	960
301	<u>N P L L Y Y F A</u> G E N F K D R L K S A L	320
961	AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTG	1020
321	R K G H P Q K A K T K C V F P V S V W L	340
1021	AGAAAGGAAACAAGAGTATAA	1041
341	R K E T R V	346

FIG. 7

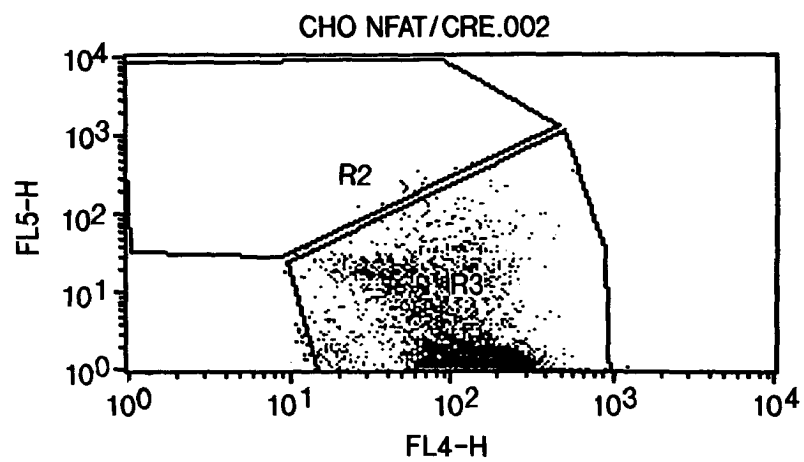


FIG. 8

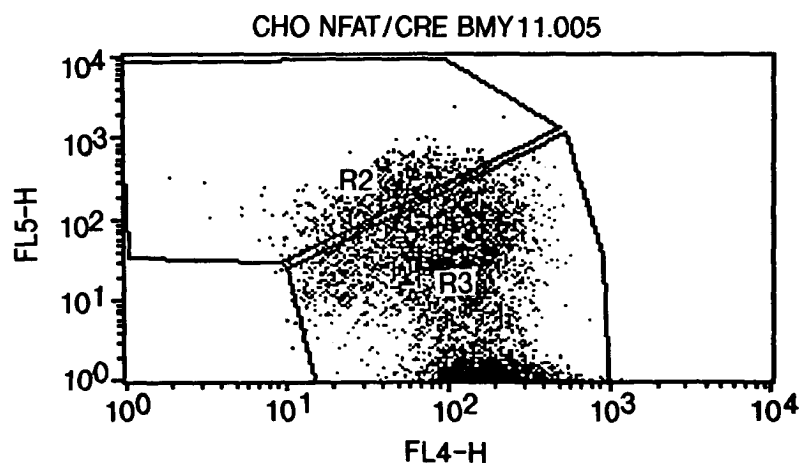


FIG. 9

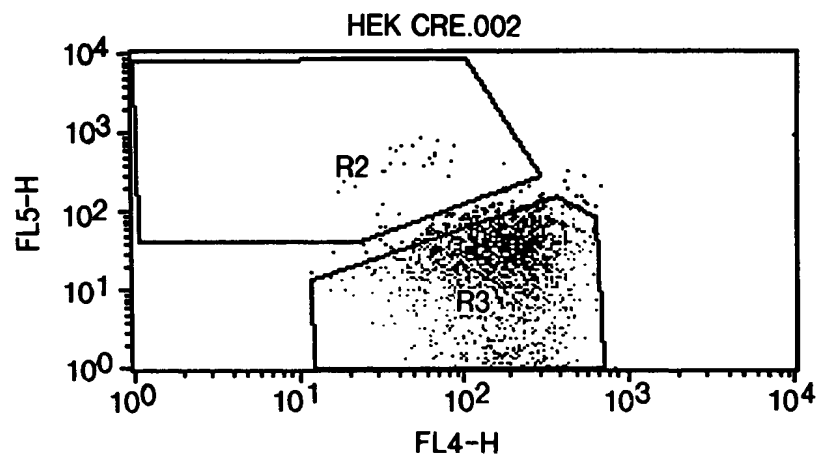


FIG. 10

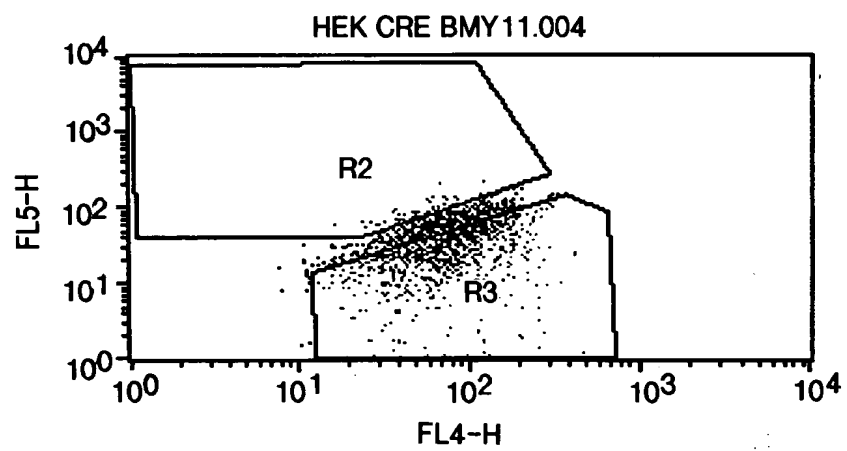


FIG. 11

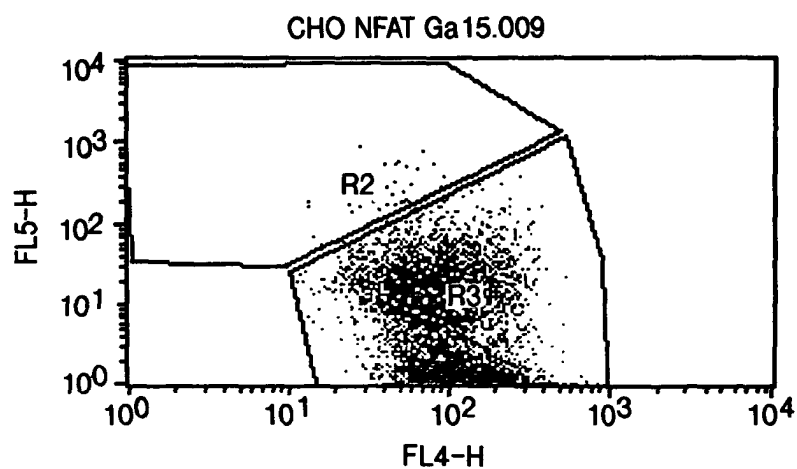


FIG. 12

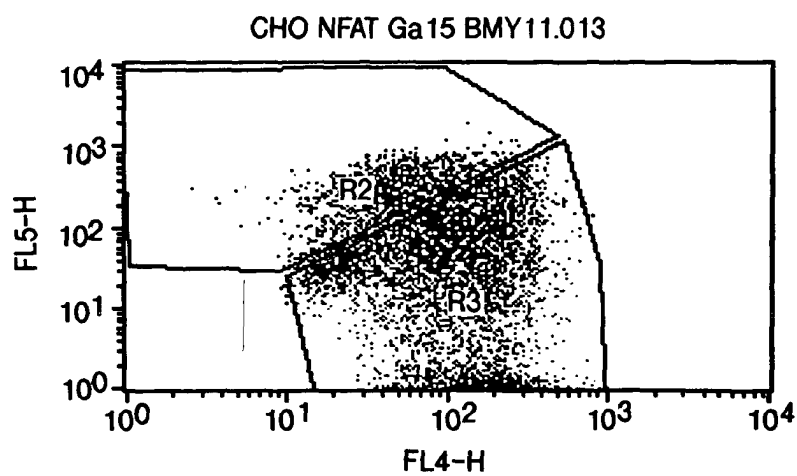
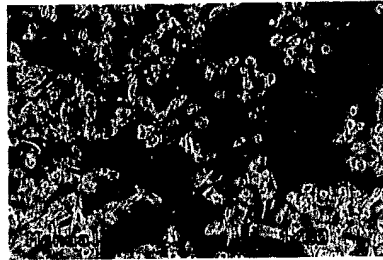


FIG. 13

Cho NFAT Gal15 Control (Fluorescent vs. Bright Field)



Cho NFAT Gal15 BMY11 (Fluorescent vs. Bright Field)

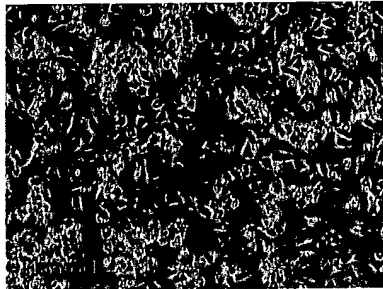
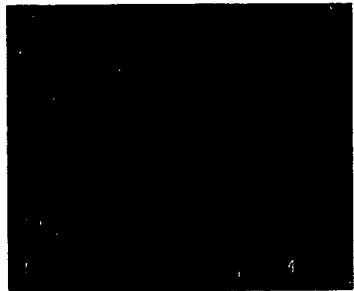


FIG. 14a

Cho-NFAT CRE

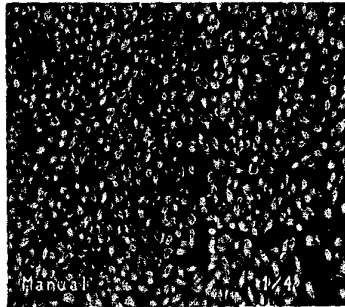


FIG. 14b

Cho-NFAT CRE + F/T/P

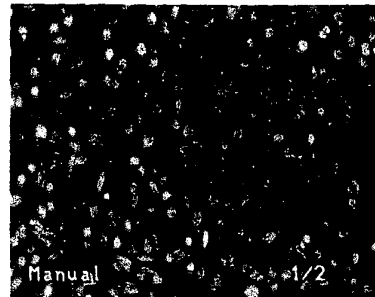


FIG. 14c

Cho-NFAT CRE oGPCR-Intermediate

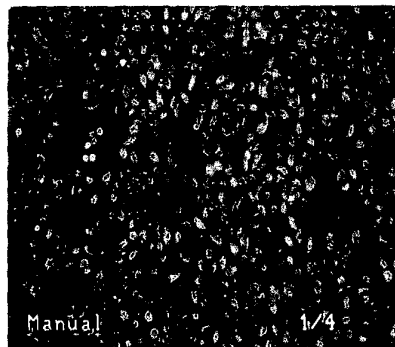


FIG. 14d

Cho-NFAT CRE oGPCR High

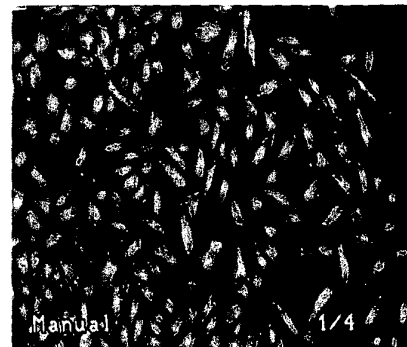


FIG. 15A

1	ATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT	60
1	M S L Q P S I S V S E M E P N G T F S N	20
61	AACAACAGCAGGAAGTGCACAATTGAAAACCTCAAGAGAGAATTTTCCCAATTGTATAT	120
21	N N S R N C T I E N F K R E F F P I V Y	40
121	CTGATAATATTTTCTGGGGAGTCTTGGGAAATGGGTTGTCCATATATGTTTCTCCTGCAG	180
41	L I I F F W G V L G N G L S I Y V F L Q	60
181	CCTTATAAGAAGTCCACATCTGTGAACGTTTTCATGCTAAATCTGGCCATTTCAGATCTC	240
61	P Y K K S T S V N V F M L N L A I S D L	80
241	CTGTTTCATAAGCAGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA	300
81	L F I S T L P F R A D Y Y L R G S N W I	100
301	TTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAGT	360
101	F G D L A C R I M S Y S L Y V N M Y S S	120
361	ATTTATTTCTGACCGTGCTGAGTGTGTGCGTTTCTGGCAATGGTTCACCCCTTTTCGG	420
121	I Y F L T V L S V V R F L A M V H P F R	140
421	CTTCTGCATGTCAACAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT	480
141	L L H V T S I R S A W I L C G I I W I L	160
481	ATCATGGCTTCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTACACA	540
161	I M A S S I M L L D S G S E Q N G S V T	180
541	TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACATATATGCCC	600
181	S C L E L N L Y K I A K L Q T M N Y I A	200
601	TTGGTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATT	660
201	L V V G C L L P F F T L S I C Y L L I I	220
661	CGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCA	720
221	R V L L K V E V P E S G L R V S H R K A	240
721	CTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTTCTGCCCCTATCACACA	780
241	L T T I I I T L I I F F L C F L P Y H T	260
781	CTGAGGACCGTCCACTTGACGACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAA	840
261	L R T V H L T T W K V G L C K D R L H K	280
841	GCTTTGGTTATCACACTGGCCTTGGCAGCAGCCAATGCCTGCTTCAATCCTCTGCTCTAT	900
281	A L V I T L A L A A A N A C F N P L L Y	300

FIG. 15B

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901 TACTTTGCTGGGGAGAATTTTAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA 960
301 Y F A G E N F K D R L K S A L R K G H P 320

961 CAGAAGGCAAAGACAAAGTGTGTTTTCCCTGTTAGTGTGTGGTTGAGAAAGGAAACAAGA 1020
321 Q K A K T K C V F P V S V W L R K E T R 340

1021 GTATAA 1026
341 V 341
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